

## FIG. 1

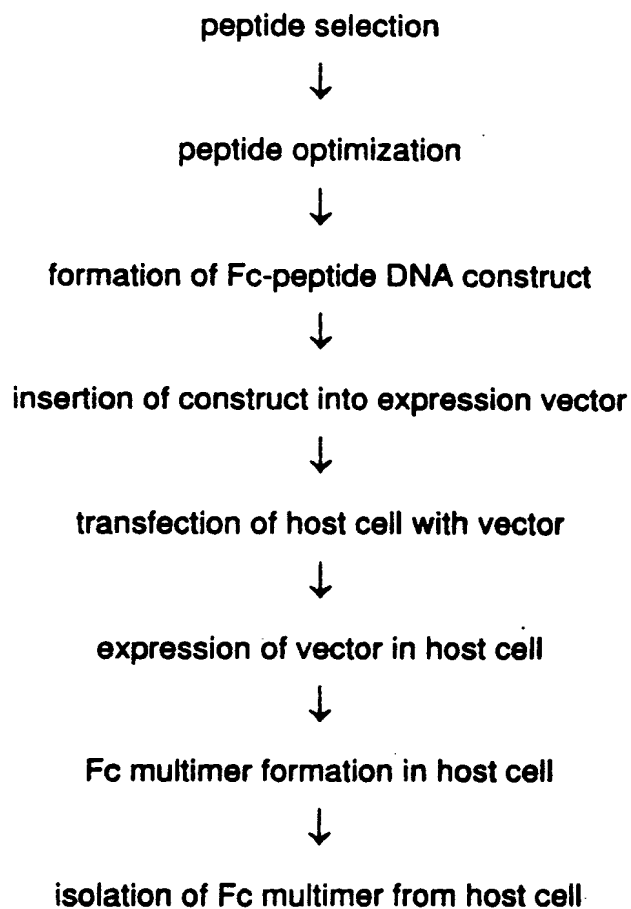


FIG. 2A

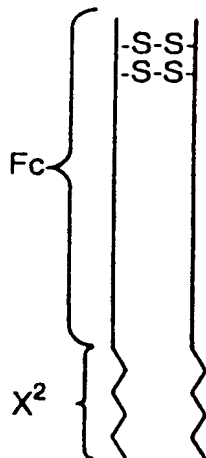


FIG. 2B

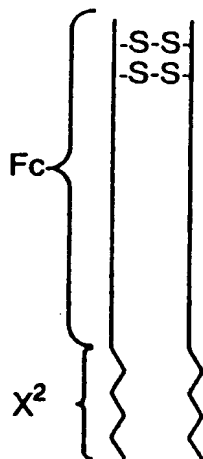


FIG. 2C

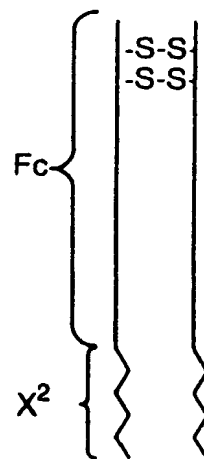


FIG. 2D

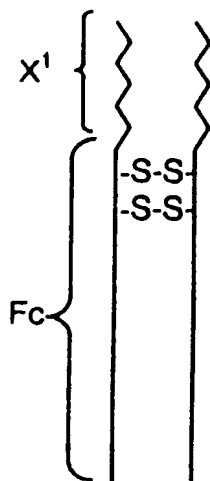


FIG. 2E

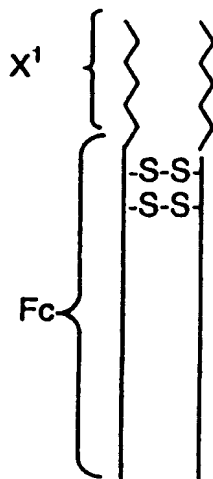


FIG. 2F

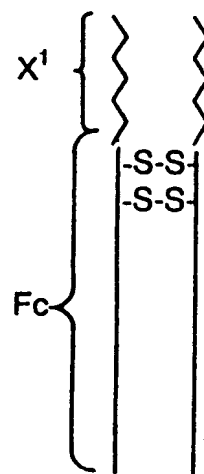


FIG. 3A

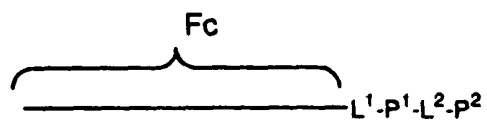


FIG. 3B

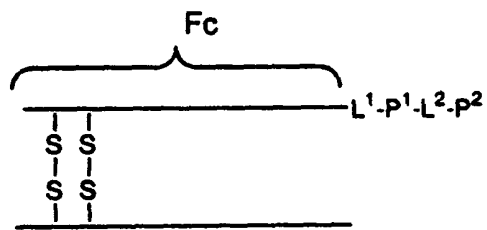
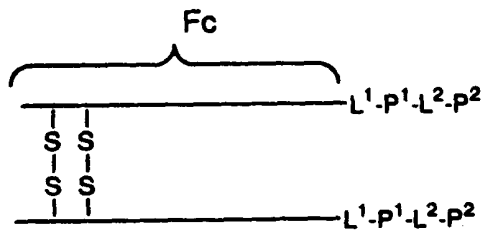


FIG. 3C



# FIG. 4

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ATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 -----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a      D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTCCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCAGAGGTTGTTTCGGGAGGGTTCGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTCAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAACACAAGACCACGCCCTCCCGTGTCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG

a      E W E S N G Q P E N N Y K T T P P V L D -

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q -

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAAGAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K -

AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

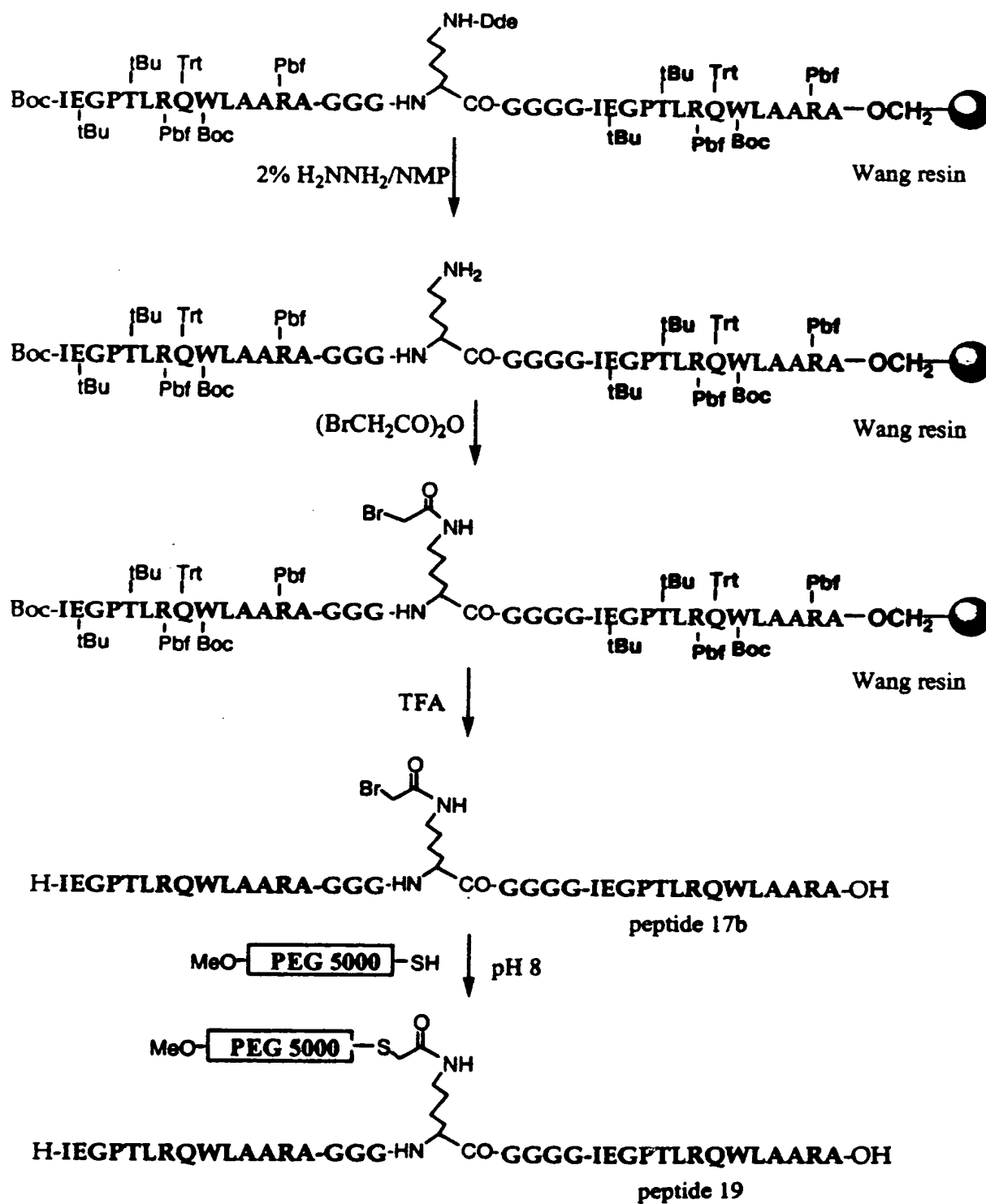
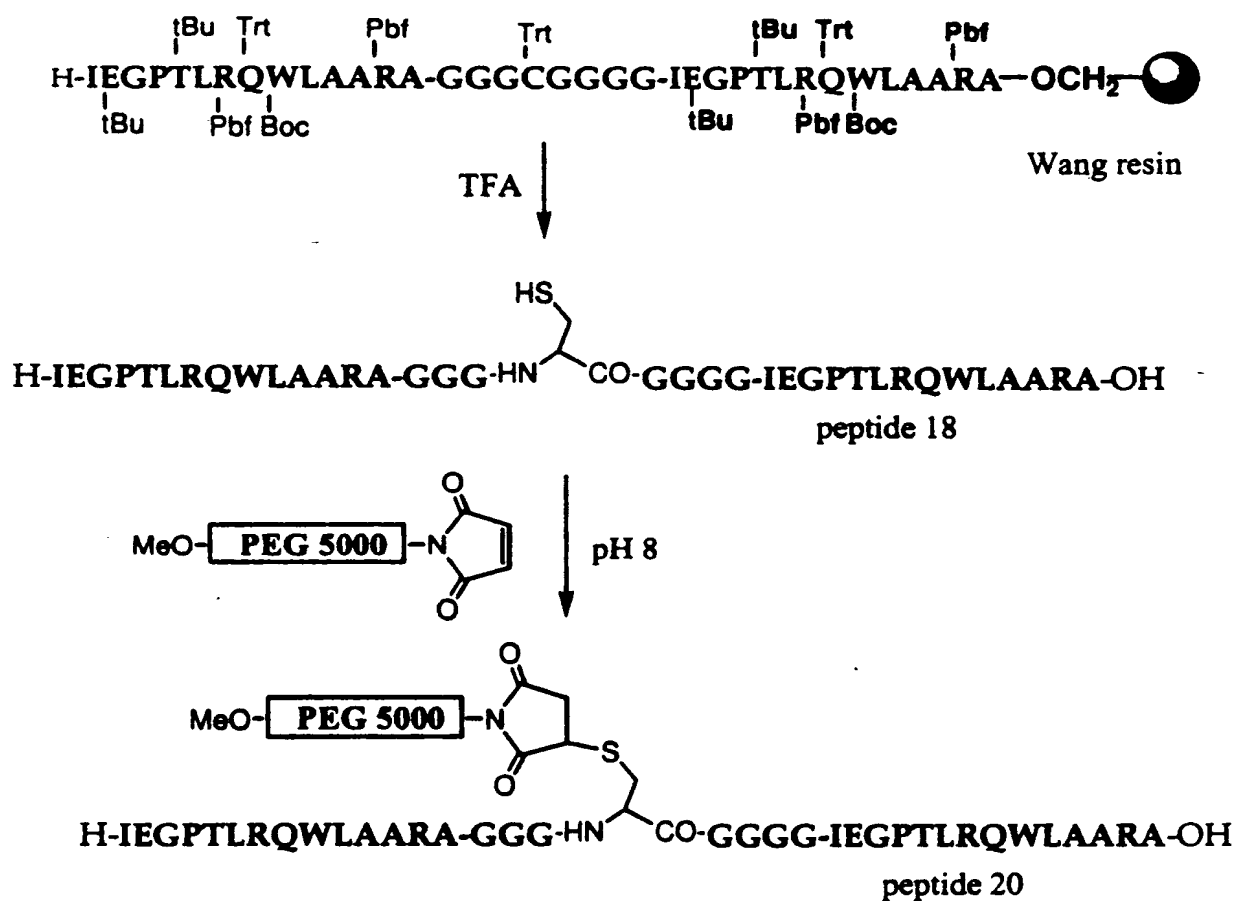


FIG. 6



XbaI  
|

1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60  
+-----+-----+-----+-----+-----+-----+  
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG  
M D K T H T C P -

61 CACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC 120  
+-----+-----+-----+-----+-----+-----+  
GTGGAACAGGTCGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG  
P C P A P E L L G G P S V F L F P P K P -

121 CCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180  
+-----+-----+-----+-----+-----+-----+  
GGTTCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGCACCACCACCTGCACT  
K D T L M I S R T P E V T C V V V D V S -

181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240  
+-----+-----+-----+-----+-----+-----+  
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC  
H E D P E V K F N W Y V D G V E V H N A -

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA 300  
+-----+-----+-----+-----+-----+-----+  
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT  
K T K P R E E Q Y N S T Y R V V S V L T -

301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCCTCAACAAAG 360  
+-----+-----+-----+-----+-----+-----+  
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTTACGTTCCAGAGGTTGTTTC  
V L H Q D W L N G K E Y K C K V S N K A -

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACAC 420  
+-----+-----+-----+-----+-----+-----+  
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG  
L P A P I E K T I S K A K G Q P R E P Q -

421 AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT 480  
+-----+-----+-----+-----+-----+-----+  
TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA  
V Y T L P P S R D E L T K N Q V S L T C -

481 GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540  
+-----+-----+-----+-----+-----+-----+  
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG  
L V K G F Y P S D I A V E W E S N G Q P -

541 CGGAGAACAAC TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT 600  
+-----+-----+-----+-----+-----+-----+  
GCCTCTTGTGTGATGTTCTGGTGCAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA  
E N N Y K T T P P V L D S D G S F F L Y -

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660  
+-----+-----+-----+-----+-----+-----+  
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCCTCGTCCCCTTG CAGAAGAGTACGAGGC  
S K L T V D K S R W Q Q G N V F S C S V -

661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720  
+-----+-----+-----+-----+-----+-----+  
ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT  
M H E A L H N H Y T Q K S L S L S P G K -

721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTT 780  
+-----+-----+-----+-----+-----+-----+  
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCAGCAGCACGAA  
G G G G G I E G P T L R Q W L A A R A \* -

BamHI  
|

781 AATCTCGAGGATCC 794  
TTAGAGCTCCTAGG

FIG. 6

XbaI  
|

1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC 60  
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTGTAGTGTGTACAG  
M D K T H T C P

61 CACCTTGTCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC 120  
GTGGAACAGGTGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAGGGGGTTTTG  
P C P A P E L L G G P S V F L F P P K P

121 CCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGGACGTGA 180  
GGTTCCTGTGGGAGTACTAGAGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT  
K D T L M I S R T P E V T C V V V D V S

181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240  
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC  
H E D P E V K F N W Y V D G V E V H N A

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA 300  
GGTTCGTGTTTCGGCGCCCTCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT  
K T K P R E E Q Y N S T Y R V V S V L T

301 CCGTCTGTCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAG 360  
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGGTTGTTTC  
V L H Q D W L N G K E Y K C K V S N K A

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420  
GGGAGGGTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG  
L P A P I E K T I S K A K G Q P R E P Q

421 AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCTGACCT 480  
TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGA  
V Y T L P P S R D E L T K N Q V S L T C

481 GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540  
CGGACCAGTTTCCGAAGATAGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG  
L V K G F Y P S D I A V E W E S N G Q P

541 CGGAGAACAACACTACAAGACCACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTCTCT 600  
GCCTCTTGTGATGTTCTGGTCCGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA  
E N N Y K T T P P V L D S D G S F F L Y

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660  
TGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC  
S K L T V D K S R W Q Q G N V F S C S V

661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720  
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGAGAGGGACAGAGGCCCAT  
M H E A L H N H Y T Q K S L S L S P G K

721 AAGTGAGGAGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTG 780  
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTACCGACCGACGAGCAGCAGC  
G G G G G I E G P T L R Q W L A A R A G

781 GTGGTGGAGGTGGCGCGGAGGTATTGAGGGCCCAACCCTTCGCCAATGGCTTGCAGCAC 840  
CACCACCTCCACCGCGCCTCATAACTCCCGGTTGGGAAGCGGTTACCGAACGTCTGTG  
G G G G G G G I E G P T L R Q W L A A R

BamHI  
|

841 GCGCATAACTCGAGGATCCG 861  
CGCGTATTAGAGCTCCTAGGC





# FIG. 10

XbaI  
|  
1 TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60  
AGATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG  
M I E G P T L R -

61 GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCGGTGGGGACAAAACCTCACACATGTCCAC 120  
CAGTCACCGACCGACGAGCAGCACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG  
Q W L A A R A G G G G G D K T H T C P P -

121 CTTGCCCAGCACCTGAACCTCGGGGGGACCGTCAGTTTTCTCTTCCCCCAAAACCCA 180  
GAACGGGTCGTGGACTTGAGGACCCCCCTGCGAGTCAAAGGAGAAGGGGGGTTTTGGGT  
C P A P E L L G G P S V F L F P P K P K -

181 AGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCC 240  
TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCTGCACTCGG  
D T L M I S R T P E V T C V V V D V S H -

241 ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA 300  
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT  
E D P E V K F N W Y V D G V E V H N A K -

301 AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCG 360  
TCTGTTTCGCGGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGAGGAGTGGC  
T K P R E E Q Y N S T Y R V V S V L T V -

361 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC 420  
AGGACGTGGTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTGTTTTCGGG  
L H Q D W L N G K E Y K C K V S N K A L -

421 TCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG 480  
AGGGTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC  
P A P I E K T I S K A K G Q P R E P Q V -

481 TGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCC 540  
ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG  
Y T L P P S R D E L T K N Q V S L T C L -

541 TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG 600  
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTGCGGC  
V K G F Y P S D I A V E W E S N G Q P E -

601 AGAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTTACA 660  
TCTTGTGATGTTCTGGTGGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGT  
N N Y K T T P P V L D S D G S F F L Y S -

661 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA 720  
CGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCCCTTGCAGAAGAGTACGAGGCACT  
K L T V D K S R W Q Q G N V F S C S V M -

721 TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT 780  
ACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA  
H E A L H N H Y T Q K S L S L S P G K \* -

BamHI  
|  
AATGGATCC  
781 TTACCTAGG

FIG.11

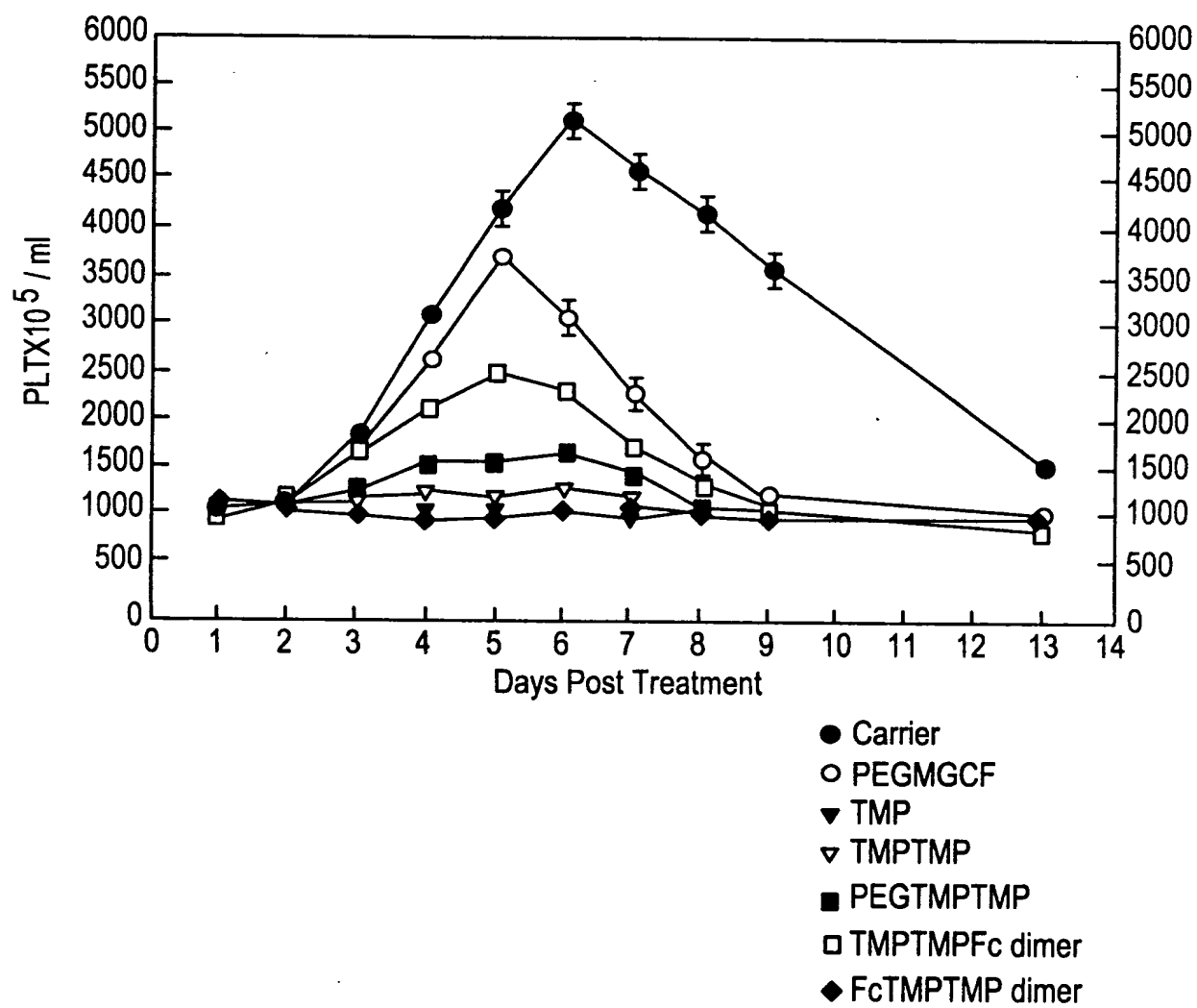
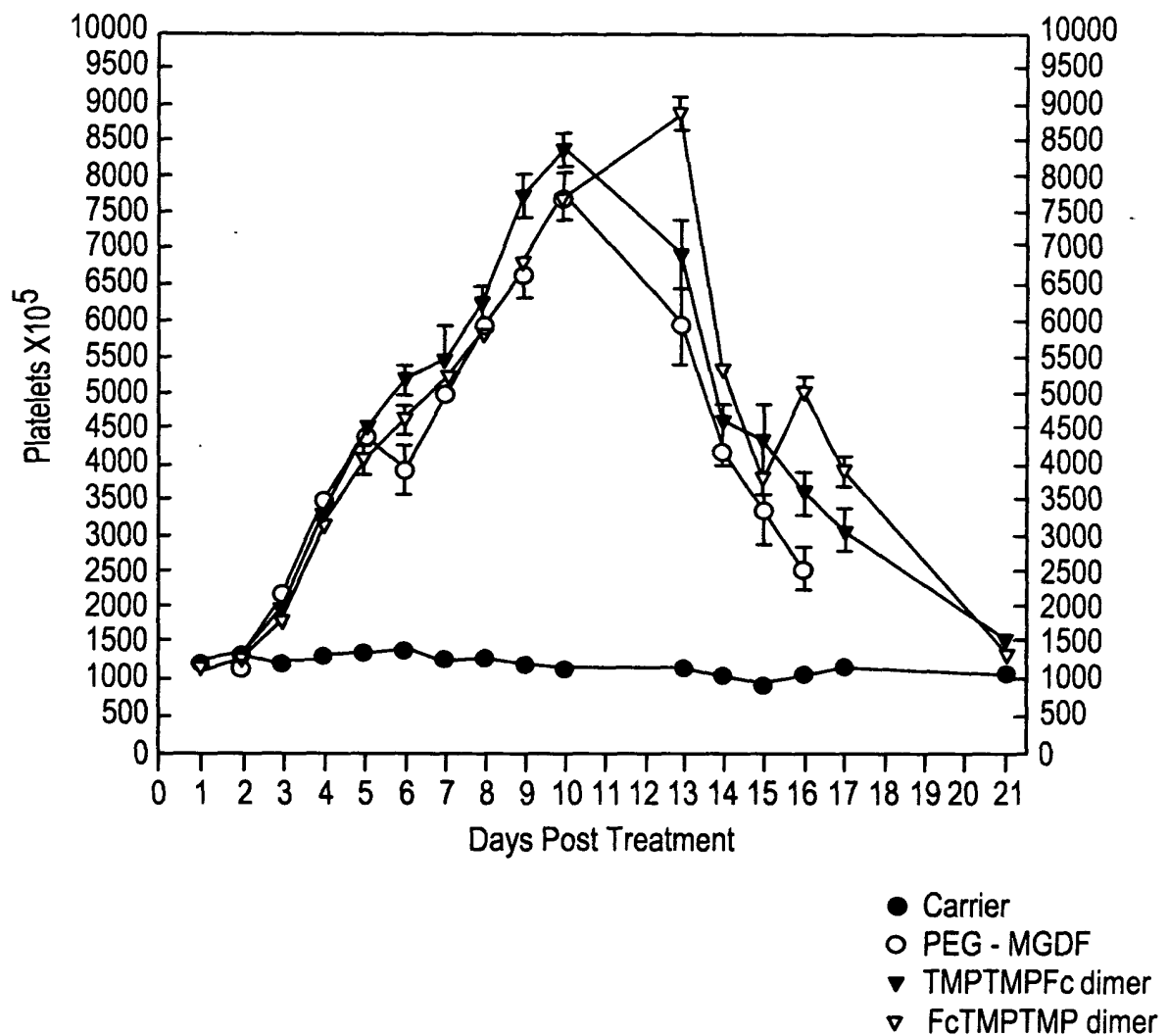


FIG.12



## FIG. 13

XbaI  
|  
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC 60  
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG  
CACCTTGTCCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAC  
61 GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTGT 120  
P C P A P E L L G G P S V F L F P P K P  
CCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA  
121 GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT 180  
K D T L M I S R T P E V T C V V V D V S  
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG  
181 CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC 240  
H E D P E V K F N W Y V D G V E V H N A  
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA  
241 GGTTCTGTTTGGGCGCCCTCTCTCGTCATGTTGTCTGTCATGGCACACCAGTCGCAGGAGT 300  
K T K P R E E Q Y N S T Y R V V S V L T  
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG  
301 GGCAGGACGTGGTCTCTGACCGACTTACCGTTCCTCATGTTTCACGTTCCAGAGGTTGTTTC 360  
V L H Q D W L N G K E Y K C K V S N K A  
CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCAC  
361 GGGAGGGTGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG 420  
L P A P I E K T I S K A K G Q P R E P Q  
AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCCTGACCT  
421 TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA 480  
V Y T L P P S R D E L T K N Q V S L T C  
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC  
481 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG 540  
L V K G F Y P S D I A V E W E S N G Q P  
CGGAGAACAACATAAGACCACGCCTCCCGTGTCTGGACTCCGACGGCTCCTTCTCTCTCT  
541 GCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGA 600  
E N N Y K T T P P V L D S D G S F F L Y  
ACAGCAAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG  
601 TGTCTGTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC 660  
S K L T V D K S R W Q Q G N V F S C S V  
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA  
661 ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT 720  
M H E A L H N H Y T Q K S L S L S P G K  
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCCGTGACTTGGGTTT  
721 TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA 780  
G G G G G T Y S C H F G P L T W V C  
BamHI  
|  
781 GCAAACCGCAGGGTGGTTAATCTCGTGGATCC 812  
CGTTTGGCGTCCCAACCAATTAGAGCACCTAGG  
K P Q G G \*

FIG. 14

XbaI

1 TCTAGATTTGTTTAACTAATTAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC  
 .....+.....+.....+.....+.....+.....+.....+ 60  
 AGATCTAAACAAATTGATTAATTTCTCCTTATTGTATACCCTCCATGAATGAGAACGG  
 M G G T Y S C H .

61 ACTTCGGCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTG GGGGAGGCCGGGGGGGACA  
.....+.....+.....+.....+.....+.....+.....+ 120  
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCCACCCTCCGCCCCCCTGT  
F G P L T W V C K P Q G G G G G G D K .

AAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGACCCTCAGTTTTC  
121 .....+.....+.....+.....+.....+.....+.....+ 180  
TTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAGG  
T H T C P P C P A P E L L G G P S V F I .

181 TCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCG  
.....+.....+.....+.....+.....+.....+.....+ 240  
AGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTAACG  
F P P K P K D T L M I S R T P E V T C V .

241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG  
 .....+.....+.....+.....+.....+.....+.....+ 300  
 ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCCG  
 V V D V S H E D P E V K F N W Y V D G V .

TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG  
.....+.....+.....+.....+.....+.....+.....+.....  
ACCTCCACGTATTACGGTTCTGTTTTCGGCGCCCTCCTCGTCATGTTGTCTGTCATGGCAC      360  
E V H N A K T K P R E E O Y N S T Y R V .

361 TGGTCAGCGTCCCTACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA 420  
.....+.....+.....+.....+.....+.....+.....+  
ACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTCTCATGTTACAGT  
V S V L T V L H Q D W L N G K E Y K C K .

421 AGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGC 480  
 .....+.....+.....+.....+.....+.....+.....+  
 TCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG  
 V S N K A L P A P I E K T I S K A K G Q -

[illegible][illegible]

601 AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG  
 .....+.....+.....+.....+.....+.....+.....+ 660  
 TCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTTCGGAGGGCACGACCTGAGGCTGC  
 S N G Q P E N N Y K T T P P V L D S D G .

661 GCTCCTTCTTCTCTACAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACG 720  
 .....+.....+.....+.....+.....+.....+.....+  
 CGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCCTCGTCCCTTGC  
 S F F L Y S K L T V D K S R W Q Q G N V .

721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT 780  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+  
 AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA  
 F S C S V M H E A L H N H Y T O K S L S .

**BamHI**

781 CCCTGTCTCCGGGTAAATAATGGATCC 807  
 .....+.....+.....  
 GGGACAGAGGCCCATTTATTACCTAGG  
 L S P G K \*



# FIG. 16

XbaI  
 |  
 1 TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60  
 AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCTGTTTGTAGTGTGTACAG  
 M D K T H T C P -

61 CACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCCTCTTCCCCCAAAAC 120  
 GTGGAACGGGTCTGTTGACTTGAAGACCCCTGGCAGTCAAAGGAGAAGGGGGTTTTG  
 P C P A P E L L G G P S V F L P P P K P -

121 CCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180  
 GGTTCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGCACCACCACCTGCCT  
 K D T L M I S R T P E V T C V V V D V S -

181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240  
 CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGACCTCCACGTATTAC  
 H E D P E V K F N W Y V D G V E V H N A -

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA 300  
 GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGTCATGGCACACCGAGTCCAGGAGT  
 K T K P R E E Q Y N S T Y R V V S V L T -

301 CCGTCTGTCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG 360  
 GGCAGGACGTGGTCTGACCGACTTACCGTTCCCTCATGTTACGTTCCAGAGGTTGTTTC  
 V L H Q D W L N G K E Y K C K V S N K A -

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420  
 GGGAGGGTCGGGGGTAGCTCTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTGGTG  
 L P A P I E K T I S K A K G Q P R E P Q -

421 AGGTGTACACCCTGCCTCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGACCT 480  
 TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCCGACTGGA  
 V Y T L P P S R D E L T K N Q V S L T C -

481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540  
 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG  
 L V K G F Y P S D I A V E W E S N G Q P -

541 CGGAGAACAACACTACAAGACCCACGCTCCCGTGTGACTCCGACGGCTCCTTCTCCTCT 600  
 GCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA  
 E N N Y K T T P P V L D S D G S F F L Y -

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTTCTCTCATGCTCCG 660  
 TGTCTGTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC  
 S K L T V D K S R W Q Q G N V F S C S V -

661 TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTA 720  
 ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT  
 M H E A L H N H Y T Q K S L S P G K -

721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780  
 TTCCACCTCCACCACCGCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCAAA  
 G G G G G G G T Y S C H F G P L T W V C -

781 GCAAACCGCAGGGTGGCGGGCGGGCGGGGGTGTACCTATTCTGTCAATTTGGCCCCG 840  
 CGTTTGGCGTCCACCGCCGCGCGCGCCGACCATGGATAAGGACAGTAAACCGGGCG  
 K P Q G G G G G G G G G T Y S C H F G P L -

BamHI  
 |  
 841 TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC 884  
 ACTGGACCCATACATTGGTGTCCCCCAATTAGAGCTCCTAGG  
 T W V C K P Q G G \*



# FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-  
 (position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-  
 -GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTCCGAGTCAGCTTTCTGA-

-GGGCCTTTCGTTTTATCTGTTGTTTGTCCGTGAACGCTCTCCTGAGTAGGACAAATCCGC-  
 -CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCTGTTTAGGCG-

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC-  
 -GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCCTCCACCGCCCGTCTGCGGGCG-

-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT-  
 -GTATTTGACGGTCCGTAGTTTAATTCGTCTCCGGTAGGACTGCCTACCGGAAAAACGCA-

AatII

-TTCTACAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-  
 -AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC-  
 -AAAATTTTCATACCCGTTAGTTAACGAGGACAATTTTAAACGAAATCTTTATGAAACCGTCG-

-GGTTTGTGTTGATTGAGTTTCATTTGCGCATTTGGTTAAATGGAAAGTGACCGTGCGCTTAC-  
 -CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCTTCGCATGCCCACGCTAAAC-  
 -ATGTCGGATTATAAAAACCTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-

-ATTCTTTTTCTCTTTTGTTTAAATCGTTGTTGATTTATTATTTGCTATATTTATTTTTC-  
 -TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA-  
 -CTATTAATAGTTGATCTCTTCTTGTAAATTACCATACAAGTATGTGCGTACATTTTTAT-

-AACTATCTATATAGTTGTCTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-  
 -TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA-

-TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA-  
 -ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-

-TTACATTTGGAGATTTTTTATTTACAGCATTTGTTTTCAAATATATTCCAATTAATCGGTG-  
 -AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTAAATTAGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-  
 -TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-

-AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-  
 -TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACCTTATAGTCTAAATTGGTATC-

-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-  
 -TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC-

-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-  
 -TATTCGTAACCTAATTATAGTAATAACGAAGATGTCCGAAATTAATAAATTAATAAGACA-

-AAGTGTCGTCGGCATTTATGCTTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG-  
 -TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-

-GCAAGTTTTGCGTGTTATATATCATTAACCGGTAATAGATTGACATTTGATTCTAATAA-  
 -CGTTCAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

## FIG. 17B

- ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -  
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -  
  
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -  
- ATCCTAGCATGTCCAAATGCGTTCCTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -  
  
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -  
- GATCTAAACAAAATTGATTAATTTCCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -  
  
- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -  
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -  
  
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -  
- CTTCTTCTTCTTCTTTTCGGGCTTTCCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -  
  
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -  
- TGATCGTATTGGGGAACCCCGAGATTTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -  
  
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]  
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

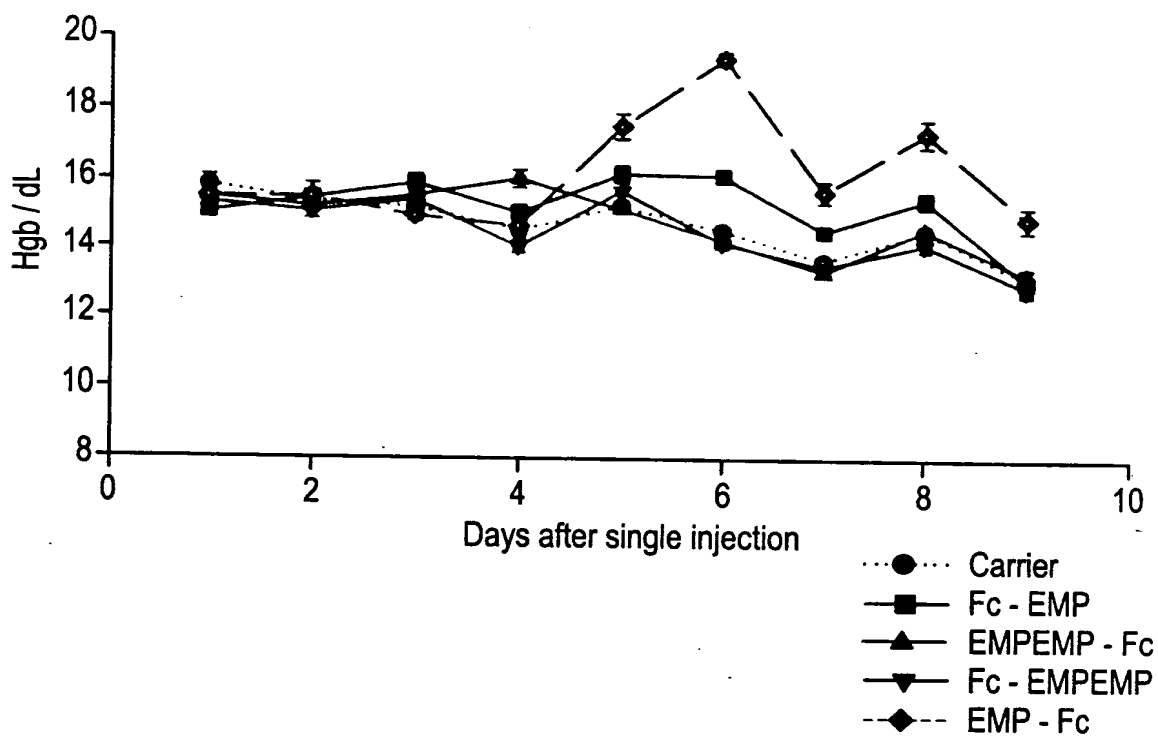


FIG.18A - 2

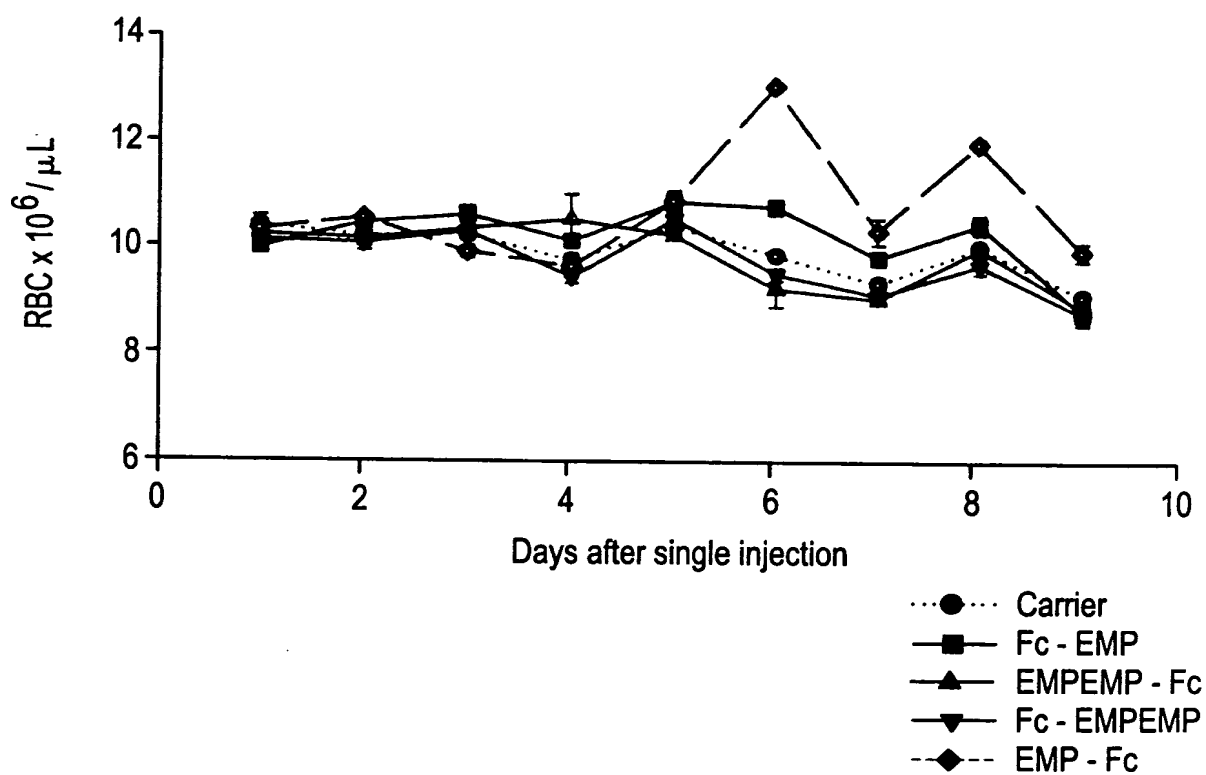


FIG.18A - 3

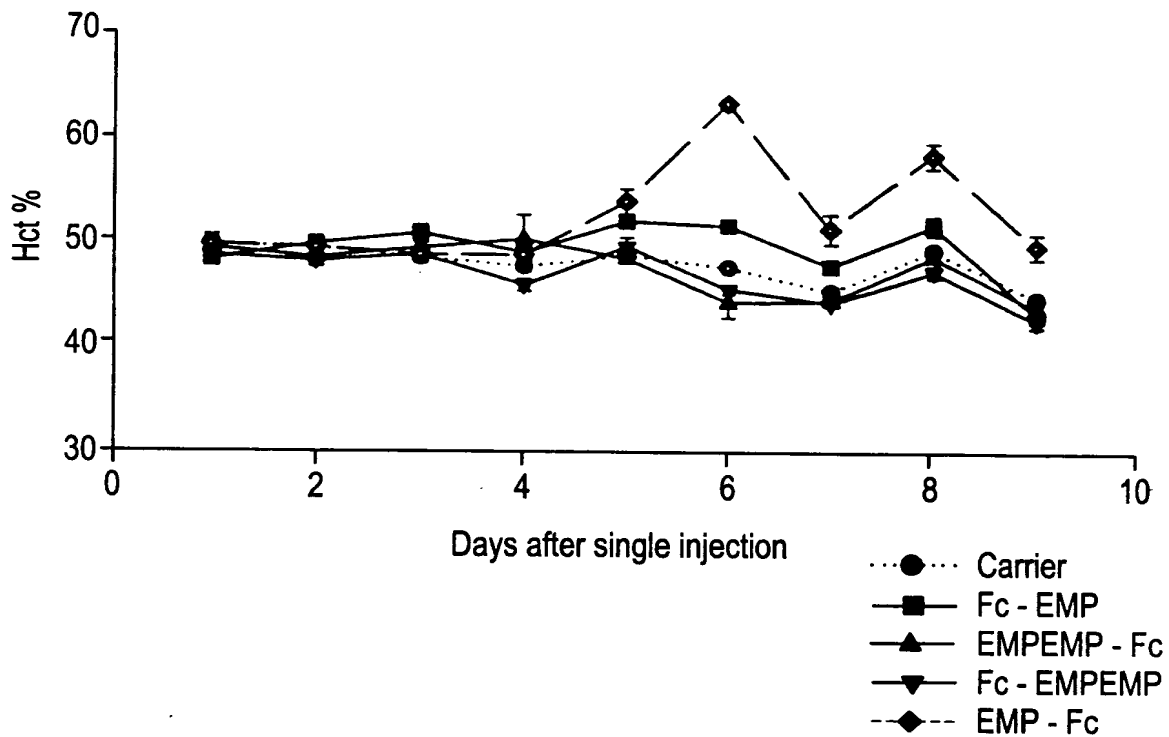


FIG.18B - 1

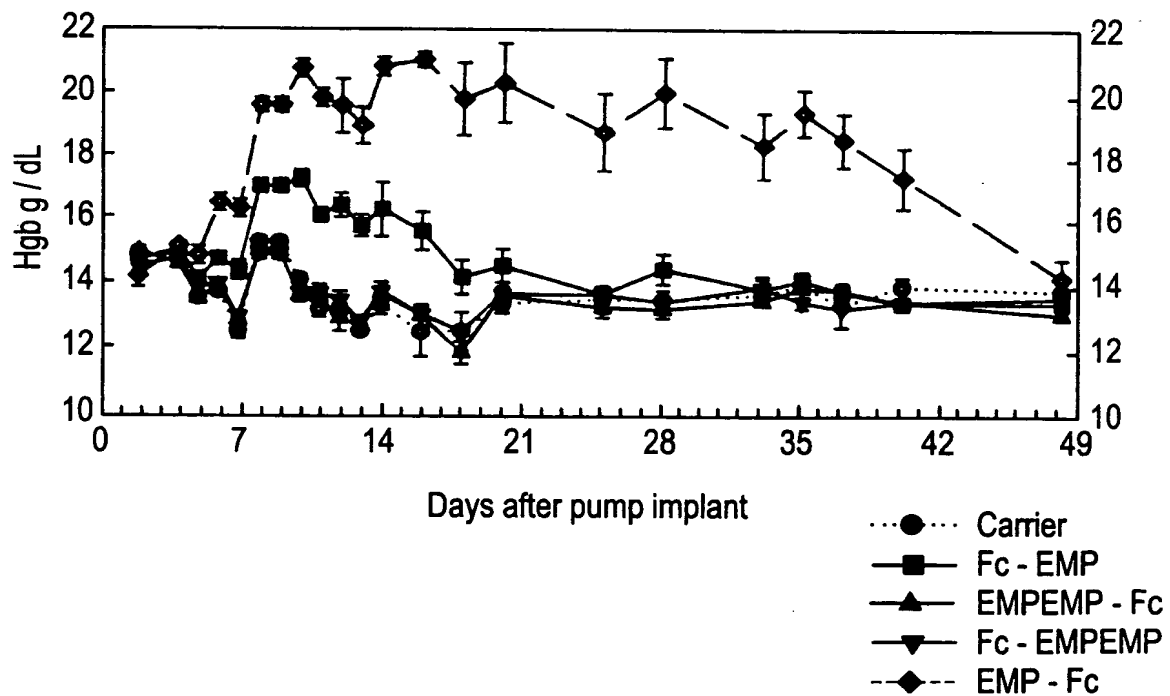


FIG.18B - 2

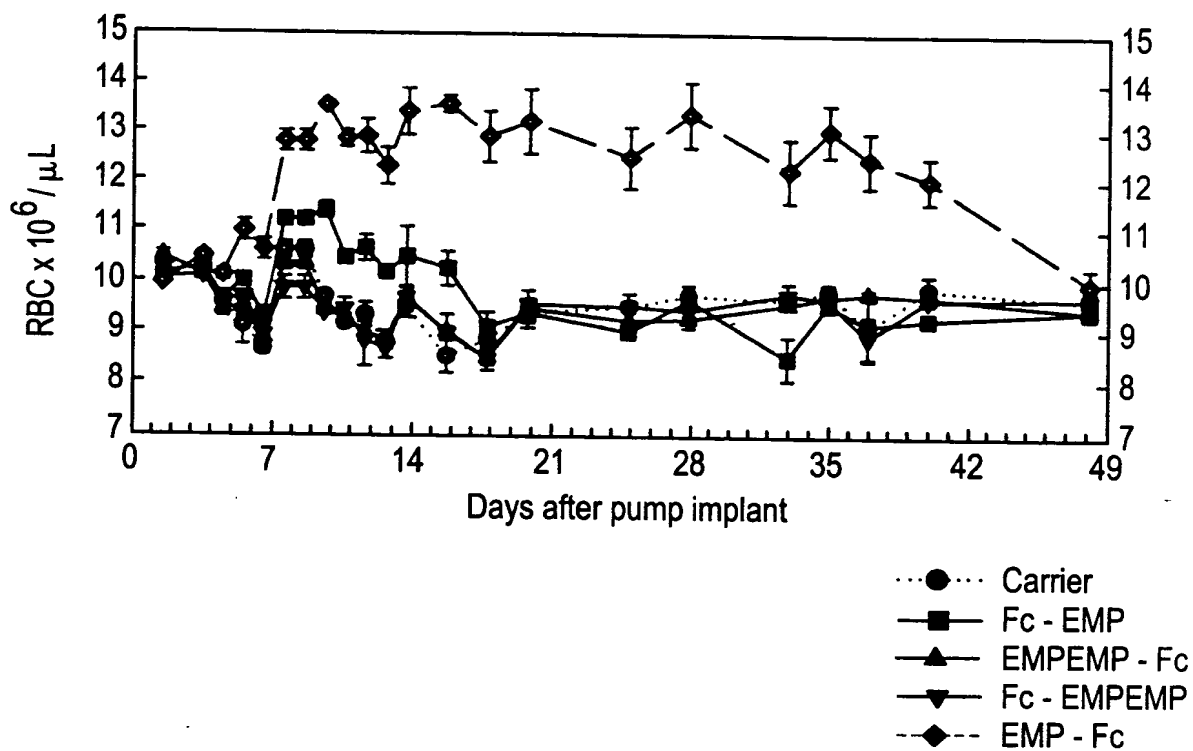
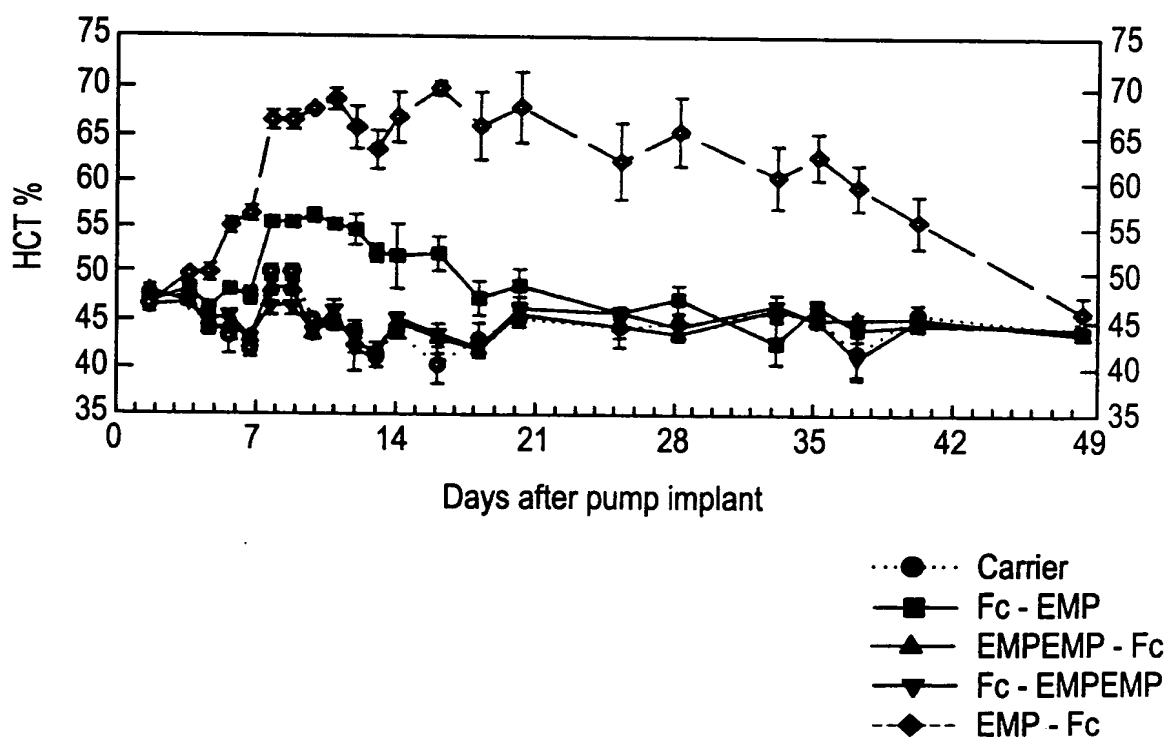


FIG.18B - 3



# FIG. 19A

NdeI  
|  
1 CATATGGACAAAACACACATGTCCACCTTGTCCAGCTCCGGAACCTCGGGGGGACCG  
-----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
-----+-----+-----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
-----+-----+-----+-----+-----+-----+-----+ 180  
CAGTGACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
-----+-----+-----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
-----+-----+-----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
-----+-----+-----+-----+-----+-----+-----+ 360  
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
-----+-----+-----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
-----+-----+-----+-----+-----+-----+-----+ 480  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACACTACAAGACCACGCCTCCCGTGCTG  
-----+-----+-----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGCAG

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
-----+-----+-----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 19B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
a   Q G N V F S C S V M H E A L H N H Y T Q .

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC 720
-----+-----+-----+-----+-----+-----+
a   K S L S L S P G K G G G G G D F L P H Y .

                                     BamHI
                                     |
721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC 757
-----+-----+-----+-----+
a   K N T S L G H R P *
```

# FIG. 20A

NdeI  
|  
CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTCACCGTCCGGGTGGAGGC  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGAAGGACGGCGTGATGTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG  
a M D F L P H Y K N T S L G H R P G G G -  
GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACCTCTGGGGGGACCG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
TCAGTTTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
AGTCAAAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGCG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
CACCTCACCTCTCGTTACCCGTGCGCCTCTTGTGATGTTCTGGTGCGGAGGGCAGCAG  
a V E W E S N G Q P E N N Y K T T P P V L -



## FIG. 20B

```

601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a      D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 720
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
-----+-----+-----+-----+-----+ 761
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a      K S L S L S P G K *
```

# FIG. 21A

NdeI  
|  
CATATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG  
1 -----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTGTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC  
a M D K T H T C P P C P A P E L L G G P -  
TCAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
61 -----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
121 -----+-----+-----+-----+-----+ 180  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 -----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
241 -----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 -----+-----+-----+-----+-----+ 360  
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
361 -----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
421 -----+-----+-----+-----+-----+ 480  
TGGTTCCTGGTCCAGTCGGAAGTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGTCTG  
481 -----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGGACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 -----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 21B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  :

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a      Y  W  Q  P  Y  A  L  P  L  *
```

## FIG. 22A

NdeI  
|  
1 CATATGTTTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC 60  
-----+-----+-----+-----+-----+-----+  
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG  
a M F E W T P G Y W Q P Y A L P L G G G -  
GGTGGGGACAAAACCTCACACATGTCCACCTTGCCCAGCACCTGAACCTCTGGGGGGACCG  
61 -----+-----+-----+-----+-----+-----+ 120  
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGACCCCTGAG  
121 -----+-----+-----+-----+-----+-----+ 180  
AGTCAAAAGGAGAAGGGGGGTTTTGGGTCTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC -  
181 -----+-----+-----+-----+-----+-----+ 240  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
241 -----+-----+-----+-----+-----+-----+ 300  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
301 -----+-----+-----+-----+-----+-----+ 360  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA  
361 -----+-----+-----+-----+-----+-----+ 420  
ATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
421 -----+-----+-----+-----+-----+-----+ 480  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
481 -----+-----+-----+-----+-----+-----+ 540  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGCTG  
541 -----+-----+-----+-----+-----+-----+ 600  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -

## FIG. 22B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+
CTGAGGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757
-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   K S L S L S P G K *
```

# FIG. 23A

NdeI  
 |  
 1 CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG 60  
 -----+-----+-----+-----+-----+-----+-----+  
 GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTGCTGGACTTGAGGACCCCCCTGGC  
 a M D K T H T C P P C P A P E L L G G P -  
 TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
 61 -----+-----+-----+-----+-----+-----+-----+ 120  
 AGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
 a S V F L F P P K P K D T L M I S R T P E -  
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
 121 -----+-----+-----+-----+-----+-----+-----+ 180  
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
 a V T C V V V D V S H E D P E V K F N W Y -  
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
 181 -----+-----+-----+-----+-----+-----+-----+ 240  
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG  
 a V D G V E V H N A K T K P R E E Q Y N S -  
 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
 241 -----+-----+-----+-----+-----+-----+-----+ 300  
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
 a T Y R V V S V L T V L H Q D W L N G K E -  
 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
 301 -----+-----+-----+-----+-----+-----+-----+ 360  
 ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTGGGGGTAGCTCTTTTGGTAGAGGTTT  
 a Y K C K V S N K A L P A P I E K T I S K -  
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
 361 -----+-----+-----+-----+-----+-----+-----+ 420  
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
 a A K G Q P R E P Q V Y T L P P S R D E L -  
 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
 421 -----+-----+-----+-----+-----+-----+-----+ 480  
 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
 a T K N Q V S L T C L V K G F Y P S D I A -  
 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG  
 481 -----+-----+-----+-----+-----+-----+-----+ 540  
 CACCTCACCTCTCGTTACCCGTGCGCCTCTTGTGATGTTCTGGTGCGGAGGGCAGAC  
 a V E W E S N G Q P E N N Y K T T P P V L -  
 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
 541 -----+-----+-----+-----+-----+-----+-----+ 600  
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC  
 a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 23B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTTGGCTTGACACTG

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  V  E  P  N  C  D  -

                                           BamHI
                                           |
721 ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC
-----+-----+-----+-----+-----+-----+ 773
TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG

a      I  H  V  M  W  E  W  E  C  F  E  R  L  *
```

## FIG. 24A

NdeI  
|  
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA  
a M V E P N C D I H V M W E W E C F E R -  
CTGGGTGGTGGTGGTGGTGACAAACTCACACATGTCCACCGTGCCAGCACCTGAACTC  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
GACCCACCACCACCACCCTGTTTTGAGTGTGTACAGGTGGCAGGGTCGTGGACTTGAG  
a L G G G G G D K T H T C P P C P A P E L -  
CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCC  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGG  
a L G G P S V F L F P P K P K D T L M I S -  
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC  
a R T P E V T C V V V D V S H E D P E V K -  
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTCTGTTCGGCGCCCTCCTC  
a F N W Y V D G V E V H N A K T K P R E E -  
CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTG  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
GTCATGTTGTCTGTCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTCTGACCGAC  
a Q Y N S T Y R V V S V L T V L H Q D W L -  
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAA  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
TTACCGTTCTCATGTTCCAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT  
a N G K E Y K C K V S N K A L P A P I E K -  
ACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG  
a T I S K A K G Q P R E P Q V Y T L P P S -  
CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
GCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG  
a R D E L T K N Q V S L T C L V K G F Y P -  
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGC  
a S D I A V E W E S N G Q P E N N Y K T T -



## FIG. 24B

```

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 660
    .....+.....+.....+.....+.....+.....+
    GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC
a      P P V L D S D G S F F L Y S K L T V D K .

661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 720
    .....+.....+.....+.....+.....+.....+
    TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a      S R W Q Q G N V F S C S V M H E A L H N .

                                BamHI
                                |
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC 773
    .....+.....+.....+.....+.....+.....+
    GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a      H Y T Q K S L S L S P G K *
```

# FIG. 25A

NdeI  
 |  
 1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG 60  
 -----+-----+-----+-----+-----+-----+  
 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCTGAGGCCTTGAGGACCCCCCTGGC  
 a M D K T H T C P P C P A P E L L G G P -  
 61 TCAGTCTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGACCCCTGAG 120  
 -----+-----+-----+-----+-----+-----+  
 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
 a S V F L F P P K P K D T L M I S R T P E -  
 121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180  
 -----+-----+-----+-----+-----+-----+  
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
 a V T C V V V D V S H E D P E V K F N W Y -  
 181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240  
 -----+-----+-----+-----+-----+-----+  
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG  
 a V D G V E V H N A K T K P R E E Q Y N S -  
 241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300  
 -----+-----+-----+-----+-----+-----+  
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
 a T Y R V V S V L T V L H Q D W L N G K E -  
 301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360  
 -----+-----+-----+-----+-----+-----+  
 ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT  
 a Y K C K V S N K A L P A P I E K T I S K -  
 361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420  
 -----+-----+-----+-----+-----+-----+  
 CGGTTTCCCGTCTGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
 a A K G Q P R E P Q V Y T L P P S R D E L -  
 421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480  
 -----+-----+-----+-----+-----+-----+  
 TGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
 a T K N Q V S L T C L V K G F Y P S D I A -  
 481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG 540  
 -----+-----+-----+-----+-----+-----+  
 CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGCGGAGGGCACGAC  
 a V E W E S N G Q P E N N Y K T T P P V L -  
 541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600  
 -----+-----+-----+-----+-----+-----+  
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGGTGGCACCTGTTCTCGTCCACCGTC  
 a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 25B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A   K   S   L   S   L   S   P   G   K   G   G   G   G   G   C   T   T   H   W   G   -

      BamHI
      |
721 TTCACCCTGTGCTAATGGATCCCTCGAG
-----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC

a   F   T   L   C   *
```

# FIG. 26A

NdeI  
|  
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a M C T T H W G F T L C G G G G G D K G -

61 GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG  
-----+-----+-----+-----+-----+-----+-----+ 120  
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCC

a G G G G D K T H T C P P C P A P E L L G -

121 GGACCGTCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACC  
-----+-----+-----+-----+-----+-----+-----+ 180  
CCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGG

a G P S V F L F P P K P K D T L M I S R T -

181 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC  
-----+-----+-----+-----+-----+-----+-----+ 240  
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a P E V T C V V V D V S H E D P E V K F N -

241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC  
-----+-----+-----+-----+-----+-----+-----+ 300  
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a W Y V D G V E V H N A K T K P R E E Q Y -

301 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC  
-----+-----+-----+-----+-----+-----+-----+ 360  
TTGTCTGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTCTGACCGACTTACCG

a N S T Y R V V S V L T V L H Q D W L N G -

361 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC  
-----+-----+-----+-----+-----+-----+-----+ 420  
TTCCTCATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a K E Y K C K V S N K A L P A P I E K T I -

421 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT  
-----+-----+-----+-----+-----+-----+-----+ 480  
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA

a S K A K G Q P R E P Q V Y T L P P S R D -

481 GAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC  
-----+-----+-----+-----+-----+-----+-----+ 540  
CTCGACTGGTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG

a E L T K N Q V S L T C L V K G F Y P S D -

541 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCCTCCC  
-----+-----+-----+-----+-----+-----+-----+ 600  
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGG

a I A V E W E S N G Q P E N N Y K T T P P -

## FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a   V L D S D G S F F L Y S K L T V D K S R .
661 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
-----+-----+-----+-----+-----+-----+ 72
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a   W Q Q G N V F S C S V M H E A L H N H Y .
                                     BamHI
                                     |
721 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 763
TGCCTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   T Q K S L S L S P G K *
```